	-5	4	AG	CTG	CGG	CCC	GGT	CTG	CCA	GCC	AG/	CCC	TTT	GG#	GAF	(GAC	CCC	ACT	CCC	TGTC	
1	ΑT	GGG	000	CCC	CIG													AGC	GCT	GGCT	60
	М		-	R		-		-			_	-	-	-		V	-		L	A	
61	GC	GAC	TCT	GGC	OCA	.GGG	CAG	GCT	GCC	TGC	CTI	CCI	'GOC	CIG		IGCT	CCA	.GCC	CCA	CGGC	120
	-	T		-	Q		R	L	₽	Α	F	L	Р	-	Ξ	L	Q	P		G	
121	CI	GGT	GAA	CTG																CCC	180
	-	V	N	С	N	M	_	~	L		-	•	P	Н	F	S	A	A	••	Р	
181	CG	GGC	CAA	CGI	CAC				CTT	ACI		CAA	.CCG	CAI			CTT	'GCA	CGA	CTCT	240
	•	Α	.,	V	T	_	L	-	L	_	•	N	R	Ι	Н	Н	L	Н	D	S	
241	GA	CTT	ŒI	CCA	CCT	GT0	CAG	CCT	ACG	AAC	TCI	CAA	CCT	CAA	GTO	GAA	CTG	XXX	GCC	GGCI	300
	D	F	V	Н	L	S	S	L	R	T	L	N	L	K	W	N	С	Р	P	A	
301	GG	CCI	CAG	CCC	CAT	GCA	CIT	CCC	CTG	CCA	CAI	GAC	CAT	CGA	GCC	CAA	CAC	CTT	CCI	GGCC	360
	G	L	S	P	М	Н	F	P	С	Н	М	T	Ι	E	Р	N	T	F	L	Α	
361	GT	GCC	CAO	CCT	GGA	GGA	GCT	GAA	CCT	GAG	CTA	CAA	CAG	CAI	CAC	GAC	CGT	GCC	ŢĠĊ	CCTG	420
	V	P	Τ	L	E	E	L	N	L	S	Y	N	\$	Ι	T	T	V	Р	A	L	
421	α	CGA	CTO	CCT	CGI	GTO	CCT	GTC	GCT	GAG	COG	CAC	CAA	CAT	CCI	GGT	GCI	'AGA	CCC	CACC	480
	Р	D	S	L	V	S	L	S	L	S	R	T	N	Ι	L	V	L	D	P	T	
481	CA	OCT	CAC	TGG	CCT.	ACA	TGC	CT	GCG	CTA	CCI	GTA	CAT	GGA	TGG	CAA	CTG	CTA	CTA	CAAG	540
	Н	L	T	G	L	Н	Α	L	R	Y	L	Y	М	D	G	N	С	Y	Y	K	
541	AΑ	000	CIG	CCA	GGG	GGO	GCI	GGA	GGT	GGT	GCC	GGC	TGC	CCT	CCI	(CCC)	CCI	'GGG	CAA	CCTC	600
	N	Ρ	C	Q	G	A	L	Ε	V	V	P	G	A	L	\mathbf{L}	G	L	G	N	L	
601	AC	ACA	TCT	CTC	ACT	CAA	GTA	CAA	CAA	TCT	CAC	GGA	GGT	GCC	000	CAG	CCT	GCC	000	CAGC	660
	Τ	Н	L	S	L	K	Y	N	N	L	T	Ε	Λ	Р	R	S	L	P	P	S	
661	CT	GGA	GAO	CCT	GCT	GTT	GTC	CTA	CAA	.CCA	CAI	TGT	CAC	CCI	GAC)GOC	TGA	.GGA	CCT	GGCC	720
	L	E	T	L	L	L	S	Y	N	Н	Ι	V	Τ	L	Τ	P	E	D	L	Α	
721	ΑA	TCT	GAC	TGO	CCT	GQG	CGT	GCT	TGA	TGT	GGG	GGG	GAA	CTG	cçç	CCG	CTG	TÇA	CCA		780
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1 (X	CAA	,000	CTC	CAC	GG/	GTC	3000	AA	\GG/	ACC/	ACC(CAF	GCI	'GCZ	CTC	TGA	CAC	CTT	CAGO	840
E	3	N	5	С	R	E	С	Р	K	D	Н	P	K	L	Н	S	D	T	F	S	
1 (A (CI	GAG	Юα	CCI	CGF	VAGC	CCI	GGT	GT1	GAA	AG/	ACAC	TTC	TCI	CTA	CAA	CCI	GGA	CGCC	900
ŀ	ł	L	S	R	L	Ε	G	L	V	L	К	D	S	S	L	Y	N	L	D	А	
1 7	AG0	STG	GTI	CCC	AGG	CCI	GGA	CAC	:GCT	TOC <i>F</i>	AGT	GC]	[GG/	CCI	GAG	TGA	GAA	CTI	CCT	CTAC	960
F	2	W	F	R	G	L	D	R	L	Q	V	L	D	L	S	E	N	F	L	Y	
1 (ZΛC	TG	CAI	CAC	CAA	GAC	CAC	GGC	CTI	CCF	GGG	CCI	[GGC	:00G	ACT]g00	CAA	.GCT	CAA	CCTG	1020
)	С	Ι	T	K	T	Τ	Α	F	Q	G	L	Α	R	L	R	K	L	N	L	
1 7	(CC	TT	CAA	TTA	CCA	CAA	GAA	GGT	GTC	CTI	TGC	CCA	1001	GCA	CÇI	GGC	ACC	CIC	CTT	IGGG	1080
S	3	F	N	Y	Н	K	K	V	S	F	Α	Н	L	Н	L	Α	P	S	F	G	
1 (AC	CT	CCG	GTC	CCI	GAA	GGA	GCT	GGA	CAT	GCA	TGG	CAT	CTT	CTI	'00G	CIC	GCT	CAG	TGAG	1140
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1 A	ICC	ΆO	CT	CCA	ACC	TCT	GGT	CCA	ACT	'GCC	TAT	GCI	YOCA	GAO	CCT	GCG	CCT	GCA	GAT	GAAC	1200
Ί	•	T	L	Q	5	L	V	Q	L	P	М	L	Q	Τ	L	R	L	Q	М	N	
1 T	TC	ΆΤ	TAA	CCA	GGC	CCA	CCT	CAG	CAT	CTT	TGG	GGC	CTT	ccc	IGG	CCT	GCT	GTA	ŒT	3GAC	1260
F	,	Ι	N	Q	A	Q	L	S	Ι	F	G	Α	F	Р	G	L	L	Y	V	D	
1 0	TA	TO	3GA	CAA	CCG	CAT	CAG	ŒG	AGC	TGC	AAG	GCC	AGT	GGa	CAT	TAC	TAG	GGA:	GT(GAT	1320
I	,	S	D	N	R	I	S	G	A	A	R	Р	V	Α	Ι	T	R	E	V	D	
1 G	GT	AG	3GA	GAG	GGT	CTG	GCT	3 00	TTC	CAG	GAA	CCT	CCC	100	ACG	TCC	ACT	3GA	CAC.	ICTC	1380
G	;	R	Ξ	R	\mathbb{A}	W	L	Р	S	R	N	L	A	Р	R	Р	L	D	Τ	L	
1 0	GC	TC	AGA	GGA)	CTT	CAT	GCC	AAA	CTG	CAA	GGO	CTT	CAG	CTT	CAO	CIT	GGA	CT	GTC.	rcgg	1440
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1 A	AC	AAG	CT	GT	GAC	AAT	CCA	GTO	GGA	GAT	GTT	TGC	TCG		CTC	ACG	CCT	CGA(TG	CTG	1500
N		N	L	V	Τ	I	Q	S	Ε	М	F	A	R	L	S	R	L	Ε	С	L	
1 0	GT	CT	AG	CA	CAA	CAG	CAT	TO	CCA	GGO	GGT	CAA	TGG	ÇŢÇ	[CA	GIŢ	IGT	300		ACC	1560
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CGTCTGAGCCACAA	R N P C R E 1 CACCTGAGCCGCCTGGG H L S R L E 1 AGGTGGTTCCGAGGCCT R W F R G L 1 GACTGCATCACCAAGAC D C I T K T 1 TCCTTCAATTACCACAA S F N Y H K 1 CACCTCCGGTCCCTGAA H L R S L K 1 ACCACCCTCGACCTCT T T L Q P L 1 TTCATTAACCAGGCCCA F I N Q A Q 1 CTATCGGACAACCGCAT L S D N R I 1 GGTACGGAGAGCGTCTG G R E R V W 1 CCCTCAGAGGACTTCAT R S E D F M 1 AACAACCTGGTGACAAC	R N P C R E C 1 CACCTGAGCCCCTCGAAGG H L S R L E G 1 AGGTGGTTCCCAGGCCTGGA R W F R G L D 1 GACTGCATCACCAAGACCAC D C I T K T T 1 TCCTTCAATTACCACAAGAA S F N Y H K K 1 CACCTCCGGTCCCTGAAGGA H L R S L K E 1 ACCACCTCCGGTCCCTGAACCTCTGGT T T L Q P L V 1 TTCATTAACCAGGCCCACCT F I N Q A Q L 1 CTATCGGACAACCGCTCAGG L S D N R I S 1 GGTAGGGAGAGGGTCTGGCT G R E R V W L 1 CCCTCAGAGGACTTCATGCC R S E D F M P 1 AACAACCTGTGAGCAACACCATC	R N P C R E C P 1 CACCTGAGCCCCTCGAAGGCCT H L S R L E G L 1 AGGTGGTTCCGAGGCCTGGACGCCT R W F R G L D R 1 GACTGCATCACCAAGACCACGGC D C I T K T T A 1 TCCTTCAATTACCACAAGAAGGGT S F N Y H K K V 1 CACCTCCGGTCCCTGAAGGAGCT H L R S L K E L 1 ACCACCTCCAACCTCTGGTCCA T T L Q P L V Q 1 TTCATTAACCAGGCCCACCTCAG F I N Q A Q L S 1 CTATCGGACAACCGCTCTGCCCAC C S D N R I S G 1 GGTACGGAGAGCGTTCGCCTGCC G R E R V W L P 1 CCCTCAGAGGACTTCAIGCCAAA R S E D F M P N 1 AACAACCTGGTGACCAACAGCATCTO N N L V T I Q S 1 CGTCTGAGCCCACACACACCATCTO	R N P C R E C P K 1 CACCTGAGCCCCTGAAGGCCTGGT H L S R L E G L V 1 AGGTGGTTCCGAGGCCTGACAGGCT R W F R G L D R L 1 GACTGCATCACCACAGACCACCGCCTI D C I T K T T A F 1 TCCTTCAATTACCACAGAAGGGTGTC S F N Y H K K V S 1 CACCTCCGGTCCCTGAAGGAGCTCGAACT T T L Q P L V Q L 1 TTCATTAACCAGGCCCACCTCAGCAI F I N Q A Q L S I 1 CTATCGGACAACCGCCTCAGCCAI C S D N R I S G A 1 GGTAGGGAGAGGGTCTGGCTGCCTCC G R E R V W L P S 1 CCCTCAGAGGAGCTTCAGCCAAACT R S E D F M P N C 1 AACAACCTGTGACCAACACACACACACCCCAA	R N P C R E C P K D 1 CACCTGAGCCGCCTGAAGGCCTGGTGT H L S R L E G L V L 1 AGGTGGTTCCGAGGCCTGGACAGGCTCCA R W F R G L D R L Q 1 GACTGCATCACCAAGAAGACCACGGCCTTCCA D C I T K T T A F Q 1 TCCTTCAATTACCACAAGAAGGTGTCCTT S F N Y H K K V S F 1 CACCTCCGGTCCCTGAAGGAGCTTGCACAT H L R S L K E L D M 1 ACCACCTCCAACCTCTGGTCCAACTGCC T T L Q P L V Q L P 1 TTCATTAACCAGGCCCACCTCAGCATCTT F I N Q A Q L S I F 1 CTATCGGACAACCGCATCTGCCTGCCTGCCTTCCAG G R E R V W L P S R 1 CCCTCAGAGGAGCTTCATGCCAAACTGCAA R S E D F M P N C K 1 AACAACCTGGTGACAACAGCATCTCCAGGAATT N N L V T I Q S E M 1 CGTCTGAGCCCACACACACACACCATCCCAGGAATT N N L V T I Q S E M 1 CGTCTGAGCCCACACACACACACATCTCCCAGGAATT N N L V T I Q S E M	R N P C R E C P K D H 1 CACCTGAGCCGCCTGAAGGCCTGGTGTTGAA H L S R L E G L V L K 1 AGGTGGTTCCGAGGCCTGGACGGCTCCAAGT R W F R G L D R L Q V 1 GACTGCATCACCAAGAAGACCACGGCTTCCAGGC D C I T K T T A F Q G 1 TCCTTCAATTACCACAGAAGAGGTGTCCTTTGC S F N Y H K K V S F A 1 CACCTCCGGTCCCTGAAGGAGCTGCACATGCA H L R S L K E L D M H 1 ACCACCTCCAACCTCTGGTCCAACTGCAACTGCAATTACCACGCCCACCTCAGCATCTTTGG F I N Q A Q L S I F G 1 CTATCGGACAACCGCCTCAGCCATCTCAAG L S D N R I S G A A R 1 GGTAGGGAGAGGGTCTGCCTGCCTGCCTGCAGGAACTGCAAG G R E R V W L P S R N 1 CCCTCAGAGGACTTCAIGCCAAACTGCAAGGCACTCTCAGGAACTGCCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAACTGCAAGGCACTCCAGGAGACTGCAAGGCACTCCAGGAGACTGCAAGGCACTCCAGGAGACTGCAAGGCACTCCAGGAGACTGCAAGGCACTCCAGGAGACTGCAAGCCACACCACACACA	R N P C R E C P K D H P 1 CACCTGAGCCCCCTGAAGGCCTGGTGTTGAAAGG H L S R L E G L V L K D 1 AGGTGGTTCCGAGGCCTGGACAGGCCTCCAAGTGCT R W F R G L D R L Q V L 1 GACTGCATCACCAAGACCACCGCCTTCCAGGCCCT D C I T K T T A F Q G L 1 TCCTTCAATTACCACAGAAGGTGTGCTTTGCCCC S F N Y H K K V S F A H 1 CACCTCCGGTCCCTGAAGGACTGCACATGCATGC H L R S L K E L D M H G 1 ACCACCTCCAACCTCTGAAGCACTGCAACTGCTTTGCCT T T L Q P L V Q L P M L 1 TTCATTAACCAGGCCCACCTCAGCATCTTTGGGC F I N Q A Q L S I F G A 1 CTATCGGACAACCGCCTCACCTGCAAGGCC L S D N R I S G A A R P 1 GGTAGGGAGAGGGTCTGCCTTCCAGGAACCT G R E R V W L P S R N L 1 CCCTCCAGAGGACTTCATGCCTAAACTGCCAACCCT R S E D F M P N C K A F 1 AACAACCTGGTGACAACAGCATCTCCCAGGCAGTTTTGC N N L V T I Q S E M F A 1 CGTCTGAGCCCACACACACACACATCTCCCAGGCGGTCAACGCCTCAACGCCTCAACGCCTTCACGGAAGCTCTTCAGGGAACCTTCAACGCCTTCAACGCCCCAACACGCAACCACC	R N P C R E C P K D H P K 1 CACCTGAGCCGCCTCGAAGGCCTGGTGTTGAAAGACAC H L S R L E G L V L K D S 1 AGGTGGTTCCGAGGCTTGGACGGCTCCAAGTGCTGGA R W F R G L D R L Q V L D 1 GACTGCATCACCACAGACCACCGCCTTCCAGGCCTGCC D C I T K T T A F Q G L A 1 TCCTTCAATTACCACAGAAGGGTGCCTTTGCCCACCT S F N Y H K K V S F A H L 1 CACCTCCGGTCCCTGAAGGAGGTGTCCTTTGCCCACCT S F N Y H K K V S F A H L 1 CACCTCCGGTCCCTGAAGGAGCTGCACATGCATGCAT H L R S L K E L D M H G I 1 ACCACCTCCAACCTCTGACACTCCTATGCTCCA T T L Q P L V Q L P M L Q 1 TTCATTAACCAGGCCCACCTCAGCATCTTTGGGCCTT F I N Q A Q L S I F G A F 1 CTATCGGACAACCGCATCTGCGCGGACTTCCAGGCACTT L S D N R I S G A A R P V 1 GGTAGGGAGAGGGTCTGCCTGCCTTCCAGGAACCTCCC G R E R V W L P S R N L A 1 CCCTCCAGAGGACTTCAIGCCAAACTGCAAGGCCTTCAG R S E D F M P N C K A F S 1 AACAACCTGGTGACAACAGCAACAGCATCTCCCGGAGATGTTTGCTCG N N L V T I Q S E M F A R 1 CGTCTGAGCCCACACACACACACACACACCATCTCCCAGGCGGTCAATGCC Amended	R N F C R E C P K D H P K L 1 CACCTGAGCCCCTCGAAGGCCTGGTTGAAAGACAGTTC H L S R L E G L V L K D S S 1 AGGTGGTTCCGAGGCCTGGACAGGCTCCAAGTGCTGGACCT R W F R G L D R L Q V L D L 1 GACTGCATCACAGACCACGGCCTTCCAGGGCCTGGCCCG D C I T K T T A F Q G L A R 1 TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCCACCTGCA S F N Y H K K V S F A H L H 1 CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGCATCTT H L R S L K E L D M H G I F 1 ACCACCCTCCAACCTCTGGTCCAACTGCCTATGCTCCAGAC T T L Q P L V Q L P M L Q T 1 TTCATTAACCAGGCCCACCTCAGCATCTTTGGGCCTTCCC F I N Q A Q L S I F G A F P 1 CTATCGGACAACCGCCTAGCATGCAGCCTGCAACGCCAGGGCT L S D N R I S G A A R P V A 1 GGTAGGGAGAGCGTCCACCTCCCCCCCCCCC G R E R V W L P S R N L A P 1 COCTCAGAGGACTTCATGCCAAACTGCAGGCCTTCAGCTTCCC G R E R V W L P S R N L A P 1 COCTCAGAGGACTTCATGCCAAACTGCAGGCTTCAGCTTC R S E D F M P N C K A F S F 1 AACAACCTGGTGACAACCGCTCCAGGAGGTTTGCCCCCCTC N N L V T I Q S E M F A R L 1 CGTCTCAGCCCAACACCCCACCCCTCCCCCGGGCGTCAACGCCCCCCCC	R N F C R 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TTCATTAACCAGGCCCACCTCAGCATCTTTCGGGCCTTCCCTGGCCT F I N Q A Q L S I F G A F P G L 1 CTATCGGACAACCCCTCTGCCTCCAGGACCTCCAGGTCCC L S D N R I S G A A R P V A I T 1 GGTAGGGAGAGCGTCTGCCTGCCTTCCAGGTCC G R E R V W L P S R N L A P R P 1 CCCTCAGAGGACTTCATGCCAAACTGCAAGGCCTCACCTTCACCTTC R S E D F M P N C K A F S F T L 1 AACAACCTGGTCACAATCCCGAGATGTTTGCCGCCTCTCACGT N N L V T I Q S E M F A R L S R 1 CGTCTGAGCCACACACACACACACACTCCCCAGGGCGTCTCACGCTTCACGTT C Ammended SEC I F C M C M C M C M C M C M C M C M C M C	R N F C R E C P K D H P K L H S D 1 CACCTGAGCCGCTCGAAGGCCTGGTGTGAAAGACAGTTCTCTCTACAA H L S R L E G L V L K D S S L Y N 1 AGGTGGTTCCGAGGCCTGAAGGCTCCAAGTGCTGGACCTGAGGAAA R W F R G L D R L Q V L D L S E N 1 GACTGCATCACCAAGACCACGGCTTCCAGGGCTGGCCGACTGGCCAA D C I T K T T A F Q G L A R L R K 1 TCCTTCAATTACCACAAAAGGTGTCCTTTCCCCACCTGCACCTGGCCAC S F N Y H K K V S F A H L H L A P 1 CACCTCCGGTCCCTGAAGGACTGGACATGCATGCATCTTCTTCCCCTC H L R S L K E L D M H G I F F R S 1 ACCACCCTCCAACCTCTGGTCCAACTCCTATGCTCAGACCCTGGCCTCT T T L Q P L V Q L P M L Q T L R L 1 TTCATTAACCAGGCCCACCTCACCATCTTTCGGGCCTTCCTT	R N F C R E C P K D H P K L H S D T 1 CACCTGAGCCGCTCGAAGGCCTGGTTGAAAGACAGTTCTCTTACAAACT H L S R L E G L V L K D S S L Y N L 1 AGGTGGTTCCAAGGCCTGACAGGCTCCAAGTGCTGACCTGAGGAACT R W F R G L D R L Q V L D L S E N F 1 GACTGCATCACCAGACCACGGCCTTCCAGGGCTGACCAGCTGAGAACT D C I T K T T A F Q G L A R L R K L 1 TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCCACCTGACCTGACCTGCCCCC S F N Y H K K V S F A H L H L A P S 1 CACCTCCGGTCCCTGAAGGACTGCACTGCCACTTCTTCCCCCCCC	R N F C R E C P K D H P K L H S D T F L CACCTGAGGGGGTTGAAAGCTGGTTGAAAGAGAGTTCTCTTACAACTGGA H L S R L E G L V L K D S S L Y N L D AGGTGGTTCGAGGGCTGGAGGGCTGAAGGCTGAGGGACTGGACTGAGAACTTCCT R W F R G L D R L Q V L D L S E N F L GACTGCATCACAGAGCAGGCTTCCAGGGGCTGACCTGAGCAGGCAG	1 CACCTGAGCCSCTCGAAGGCCTGGTTGAAAGAGTTCTCTCTACAACCTGGAGGCC H L S R L E G L V L K D S S L Y N L D A 1 AGGTGGTTCCGAGGCCTGGACGGCTCCAAGTGCTGGACCTGGACGTACAACTTCCTCTAC R W F R G L D R L Q V L D L S E N F L Y 1 GACTGCATCACCAAGGCCTCCAGGCCTTCCAGGCCTGGCCGACTGGCCAAGCTCAACCTC D C I T K T T A F Q G L A R L R K L N L 1 TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCCACCTGGACCTGCACCCTCCTTTGGC S F N Y H K K V S F A H L H L A P S F G 1 CACCTCCGGTCCCTGAAGGAGCTGGACATCCATCCATCTCTTCCGCTCCCTCAGGAGC H L R S L K E L D M H G I F F R S L S E 1 ACCACGCTCCAACCTCTGGTCCAACTGCCATTGCTCAGGACCTTCCAGGATGAAC T T L Q P L V Q L P M L Q T L R L Q M N 1 TTCATTAACCAGGCCCACCTCAGGCATCTTTCGGGCCTTCCTGGACGGAC

1561	AG	CCT	GOG	GGT	GCT	GGA	CCI	GTC	CCA	CAA	CAA	GCT	GGA	CCT	GTA	TCA	CGG	GCG	CTC	GTTC	1620
	S	L	R	V	L	D	T LL	S	Н	N	K	L	D	L	Y	Н	G	R	S	F	
1621	AO	GGA	GCT	GCC	GCG	CCT	GGA	AGC	ACT	GGA	CCT	CAG	CTA	CAA	CAG	CCA	GCC	CTT	TAC	CATG	1680
	T	Ε	L	P	R	L	E	A	L	D	L	\$	Y	N	S	Q	P	F	T	M	
1681	CA	GGG	TGT	GGG	CCA	CAA	CCT	CAG	CTT	CGT	GGC	CCA	GCT	GCO	CGC	CCT	GŒ	CTA	CCT	CAGC	1740
	Q	G	V	G	Н	N	L	S	F	V	A	Q	L	P	Α	L	R	Y	L	S	
1741	CT	GGC	GCA	CAA	TGA	CAT	CCA	TAG	ŒĠ	AGT	GTC	CCA	GCA	CCT	CTG	TAG	CGC	CTC	ACT	GTGC	1800
	L	Α	Н	N	D	Ι	Н	S	R	V	S	Q	Q	L	С	S	Α	S	L	С	
1801	GO	CCT	GGA	CTT	TAG	CGG	CAA	OGA	TCT	GAG	CCG	GAT	GIG	GGC	TGA	GGG	AGA	.CCT	CTA	TCTC	1860
	Α	L	D	F	S	G	N	D	L	S	R	М	W	A	Ε	G	D	L	Y	L	
1861	CG	CTT	CTT	CCA	AGG	CCT.	AAG	AAG	ŒΙ	AGT	CTG	GCI	GGA	CCT	GTC	CCA	GAA	CCA	CCT	GCAC	1920
	R	F	F	Q	G	L	R	S	L	V	W	L	D	L	S	Q	N	Н	Ĺ	Н	
1921	AO	CCT	CCT	GCC	ACG	TGO	ÇÇT	GGA	CAA	ŒΤ	000	CAA	AAG	CCT	GAA	GCA	TCT	GCA	TCT	CCGT	1980
	T	L	L	P	R	Α	L	D	N	L	P	K	S	L	K	Н	L	Н	L	R	
1981	GA	CAA	TAA	CCT	GGC	CTT	CTT	CAA	CTG	GAG	CAG	CCI	GAC	ŒΤ	ŒΙ	GCC	CAA	.GCT	'GGA	AACC	2040
	D	N	N	L	Α	F	F	N	W	S	S	L	Ţ	L	L	P	K	L	Ε	T	
2041	CT	GGA	CTT	GGC	TGG	AAA	CCA	GCT	GAA	.GGC	CCT	'AAG	CAA	TGG	CAC	CCT	GCC	ATC	TGG	CACC	2100
	L	D	L	A	G	N	Q	L	K	A	L	S	N	G	S	L	P	S	G	T	
2101	.CA	GCT	GCG	GAG	GCT	GGA	CCT	CAG	TGG	CAA	CAG	CAT	ÇGG	CTT	TGT	GAA	000	TGG	CTT	CTTT	2160
	Q	L	R	R	L	D	L	S	G	N	S	I	G	F	V	N	P	G	F	F	
2161	GC	CCI	GGC	CAA	GCA	GTT	AGA	AGA	.GCT	CAA	CCT	'CAG	CGC	CAA	TGC	CCT	CAA	GAC	AGT	GGAG	2220
	Α	L	A	K	Q	L	Ε	Ε	L	N	L	S	Α	N	Α	L	K	Τ	V	E	
2221	CC	CTC	CIG	GTT	TGG	CTO	GAT	GGT	GGG	CAA	CCT	GAA	AGT	CCT	AGA	CGT	GAG	CGC	CAA	CCT	2280
	Р	S	W	F	G	S	M	V	G	N	L	К	V	L	D	V	S	Α	N	P	
2281	.CT	GCA	CTG	CGC	CTG	TGG	GGC	GAC	CTI	CGT	GGG	CTI	CCT					GGC	TGC	OGTG	2340
	т	Н	С	Α	C	G	A	T	F	17	G	U	ĭ	Į.	SEC	<u> </u>	$\frac{0}{0}$	O:1	10	315-2	2394)
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2341	. CC								-											CATC	2400
	P	G	L	Р	S	R	V	K	C	G	S	Р	G	Q	L	Q	G	Н	S	Ι	
2401	TT	IGC	GCA/	AGA	CT	GOG	CI	CIG	CT	GGA	TGA	GAC	CCT	CIC	GTG	GAA	CTG	TTT	TGG	CATC	2460
	Ē	Α	Q	D	L	R	L	С	L	D	Ε	Ţ	L	S	W	N	С	F	G	Ι	
2461	TO	GCT(GCI	GG0	CAT	GGO	CCT	GGG	ŒΤ	GGT	TGT	GCC	CAT	GCT	GCA	CCA	CCI	CTG	Œ	CTGG	2520
	S	L	L	A	М	Α	L	G	L	V	V	Р	M	L	Н	Н	L	С	G	W	
2521	GA	CCT	CTG	GTA	CTG	CIT	CCA	CCT	GTG	ŒΤ	GGC	CTG	CCT	GCC	CCA	CCG	AGG	GCA	GCC	GCGG	2580
	D	L	W	Υ	С	F	Н	L	C	L	Α	W	L	Р	Н	R	G	Q	R	R	
2581	GG	JGC	AGA(CGO	CI	GIT	CTA	TGA	TGC	CTT	CGT	GGI	CTT	TGA	CAA	AGC	TCA	GAG	TGC	TGTG	2640
	G	Α	D	Α	L	F	Y	D	Α	F	V	V	F	D	K	Α	Q	S	A	V	
2641	GO	CGA	CTG	GGT	GTA	CAA	CGA	GCT	GCG	GGT	GCA	GC1	GGA	GGA	GCC	CCG	TGG	GŒ	OC g	CGCA	2700
	A	D	W	V	Y	N	Ε	L	R	V	Q	L	Ε	Ε	R	R	G	R	R	A	
2701	CT	30G	CCI	GTG	CT	GGA	GGA	GOG.	AGA	CTG	GTT	ACC	TGG	CAA	GAC	GCT	CTT	CGA	GAA	CCTG	2760
	L	R	L	С	L	E	Ε	R	D	W	L	Р	G	K	Τ	L	F	E	N	L	
2761	TG	3G0	CTC	AGT	CTA	CAG	CAG	aag	CAA	GAC	CCI	GTI	TGT	GCT	GGC	CCA	CAC	CGA	.000	TGTC	2820
	W	А	S	V	Y	S	S	R	K	T	L	F	V	L	Α	Н	T	D	R	V	
2821	AG	OGG	CCT	CTT	GOG	TGO	CAG	TTT	CCT	GCT	GGC	CCA	GCA	GCG	ŒΊ	GCT	GGA	.GGA	.ccc	CAAG	2880
	S	G	L	L	R	Α	S	F	Ţ.,	L	Α	0	0	R	L	L	Ε	D	R	K	
2881	. GA	OGT	TGT	AGT	CT	GGI	GAT	ccr	GCG	αc	CGA	TGC	CIA	CCG	CTC	.COG	CTA	.CGT	'GCC	GCTG	2940
	D	V	V	V	L	V	I	L	R	р	D	Α	Y	R	S	R	Y	V	R	L	
2941	CG	CCA:	aCG	acti	- CTG	CCG	CCA	GAG	TGT	- CCT	CCT	CTG	GCC	CCA	CCA	GCC	na:	TGG	GCA	.GGGC	3000
2712	R		_								L			Н		Р	R		0		0000
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2001			W	A							T						F	Y Y		R	5000
2061	~	*-	••	* *	~																3147)
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		110.0		
SWINE	1	MCPRCTLHPLSLLVQVTALAATLAQCRLPAFLPCELQPHGLVNCNMLFLKSVPHFSAA	58	SWINE
HUMAN	1	MCP-CRSALHPISILIVQAIMIAMTIALGTI.PAFI.PCELQPHGLVWCMILFIKSVPHF3MA	59	HUMAN
MOUSE	1	MVLRRKT-LHPLSLLVQAAVIAETLALGTLPAFLPCELKPHGLVDCMIFIKSVPRFSAA	59	MOUSE
CAT	1	MCP-CHCALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAA	59	CAT
		* ******** ** .** *.************.****		
SWINE	50	APRANVI'S LILSNR HHLHDSDFVHLSS LRILNIKWVCPPAGLSPMHFPCHMI LEPNIF 1	10	QW/INE
HUMAN		APPROVIDES ISSNR I HHI HOSDFAHLPST RHI NI KWXCPPVGLSPMHFPCHMT I EPSTF 1		
MOUSE		ASCENITRISLISNRIHHLIANSDEVHILSVILROLNIKAVOPPIGLSPLHESCHMITEPRIF 1		
CAT		APROVITSTSTYSNRTHHTHDSDFVHTSSTRRTNTKWVDPPASTSPMHPPCHMTTEPHTF		
UAI	υo	* * * * * * * *** *** * * * * * * * *	13	GAI
SWINE	119	LAVPTLEELVLSYNSITTVPALPDSLVSLSLSKINTLVLDPTHLIGLHALRYLYDDQXCY 1	78	SWINE
		LAVPTIFELNISYNVIMIVPALPKSLISLSLSHTVIIMLDSASLAGLHALRFLFMDQXCY I		
MOUSE	120	LAMPITFEINLSYNGITTVPRLPSSLVNLSLSHINILVLDANSLAGLYSLRVLFMDQXCY 1	79	MOUSE
CAT	120	LA V PT LEE L N LSYNS ITT V PALPSS L V S LS L S R T N L L V L D PANLAG L H S L R F L F L D G N C Y L L L G N C M C L G N C M C L G N C M C M C M C M C M C M C M C M C M C	79	CAT
		** ******** * *** ** ** *** *** *** * *		
SWINE	179	YKNPOQGALEWPGALIGLGNLTHLSLKYNNLTEVPRSLPPSLETLLLSYNHIVTLTPED 2	38	SWINE
HUMAN	180	YKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTWPRNLPSSLEYLLLSYNRIVKLAPED 2.	39	HUMAN
MOUSE	180	YKNPCTGAVKVTPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYLLVSYNLIVKLGPED 2	39	MOUSE
CAT	180	YKNPCPQALQVAPCALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYLLLSYNHIITLAPED 2	39	CAT
		***** * * ****** ********** *** ** ** *		
SWINE	239	LANITALRYI DYGGNORRODHARNPORFOPKDHPKLHSIVIFSHLSRLEGLYI KDSSLYNI, 2	98	
0111112		Amended (SEQ ID NO:		1-298)
HUMAN	240	LANLTALRVILDVGQVCRRCDHAPNPQVECPRHFPQLHPDTFSHLSRLEGIVIKDSSLSWL 2		
		(SEQ ID NO:	-	1-299)
MOUSE	240	LANLTSLRVILDVGCNCRRCDHAPNPCTECCGCKSTHTHPETFHHLSHLEGTVIKDSSTHTL 2		1 200)
	0.40	(SEQ ID NO:		1-299)
CAT	240	LANLTALRVI.DVGGVCRCDHAPNPOJECPKGFPHLAPDIFSHINHLEGIJVIKDSSLYNI, 2		
		(SEQ ID NO:	8	1-299)

SWINE	299	DARWERGLDRIQVIDISENFLYDCITKTTAFQGLARLRKINISENYHKKVSFAHLHIAPS 358
HUMAN	300	${\tt NASWFRGLGVLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPS\ 359}$
MOUSE	300	${\tt NSSWEQGLVALSVIDLSENFLYESINHINAFQNLTRLRKINLSFNYRKKVSFARLHLASS\ 359}$
CAT	300	NPRWFHALGNIAVIDISENFIYDCITKTTAFQGLAQIRRINISFNYHKKVSFAHLHIAPS 359
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SWINE	359	FGHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLY 418
HUMAN	360	${\tt FGSLVALKELDM+GIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRY~419}$
MOUSE	360	FKNLVSLQELNMAGIFFRSLAKYTLRWLADLPKLHITLHLQMAFINQAQLSIFGTFRALRF 419
CAT	360	FGSLLSLQQLDMHGIFFRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRY 419
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SWINE	419	VDLSDNRISGAARPVAITREVDGR-ERVWLPSRNLAPRPLDTLRSEDEMPNCKAFSFTLD 477
HUMAN	420	VDLSDNRISCASELTATMGEADGG-EKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLD 478
MOUSE	420	VDLSDNRISGPSTLSEATPEEADDAEQEELLSADPHPAPLSTPASKNFMDRCKNFKFTMD 479
CAT	420	VDLSDNRISGAMELAAATGEVDGG-ERVRIPSGDLALGPPGTPSSEGFMPGCKTLNFTLD 478

SWINE	478	LSRNNLVTIQSEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVIDLSHNKLDLYHG 537
LIUMANI	470	Amended (SEQ ID NO:2 299-537) LCRINILYTYOPENFAOLSHLOCIRLSHNCISQAVNGSOFIPLIGLOVIDLSRNKIDLYHE 538
HUMAIN	4/3	[SEQ ID NO:4 300-538]
MOUSE	480	LGRANILYTIKPEMFVNISRIQCISISHNSIAQAVNGSQFIPIJINIQVIDISHNKIDLYHW 539
		(SEQ ID NO:6 300-539)
CAT	479	LSRNNLVTIQPEMFARLSRIQCILLISRNSISQAVNGSQFMPLTSLQVIDLSHVKLDLYHG 538
		(SEQ ID NO:8 300-538)

SWINE	538	RSFTELPRIEALDISYNSOPFTMOGVGHNISFVAQIPALRYLSIAHNDIHSRVSQQLCSA	597
HUMAN	539	HSFTELPRIEALDISYNSOPFGAOGYGHNFSFVAHIRTIRHISIAHNNIHSQVSQQICCT	598
MOUSE	540	KSFSELPOLQALDLGYNSOPFSIKGIGHNFSFVAHLSMIHSLSLAHNDIHTRVSSHINSN	599
CAT	539	RSFTELPRIFALDISYNSQPFSMQGVGHNLSFVAQIPALRYLSIAHNDIHSRVSQQLCCA	598
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SWINE	598	${\tt SLCALDFSGNDLSRWADGDLYLRFFQGLRSLWILDLSQNHLHTLLPRALDNLPKSLKHL}$	657
HUMAN	599	${\tt SLRAIDFSG}{\tt VALGHWARGDLYLHFFQGLSGLIWLDLSQNRLHTLIPQTLRNLPKSLQVL}$	658
MOUSE	600	${\tt SVFFIDFSGWOWERWODEGCLYLHFFQGLSGLLKLDLSQWNLHILRPQWLDWLPKSLKLL}$	659
CAT	599	${\tt SLRAIDFSGVALSRWAPGDLYLXFFRGLRSLVRLDLSQNRLHTLLPRITLDNLPKSLRLL}$	658
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SWINE	658	HLRDINNLAFFNWSSLITLLPKLETIDLAGNQLKALSNGSLP9GTQLRRLDLSGNSIGFVNP	717
HUMAN	659	RLRDNYLAFFKWWSLHFLPKLEVLDLAGNRLKALINGSLPAGTRLRRLDVSCNSISEVAP	718
MOUSE	660	${\tt SLRDNYLSFFNWISLSFLPNLEVLDLAGNQLKALINGTLPNGTLLQKLDVSSNSIVSVVP}$	719
CAT	659	RLRDNYLAFFNWSSLVILLPRIEALDLAGNQLKALSNGSLPNGTQLQRLDLSSNSISFVAS	718
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SWINE	718	GFFALAKQLEELNLSANALKTVEPSWFGSMYGNLKVLDVSANPLHCACGATFVGF1LEVQ	777
HUMAN	719	$\tt GFFSKAKELREINLSANALKIVDHSNFGPLASALQILDVSANPLHCACGAAFMDFLLEVQ$	778
MOUSE	720	AFFALAVELKEVNLSHNILKTVDRSWFGPIVMVLTVLDVRSNPLHCACGAAFVDLLLEVQ	779
CAT	719	${\tt SFFALATRLIRE} {\tt INLSANALKIVEPSWPGSLAGIIKVLDVIGNPLHCACGAAFVDFLLEVQ}$	778
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SWINE	778	AAVPGLPSRVKOGSPGQLQCHSIFAQDLRLCLDETLSWCFGISLLAMALGLVVPMLHHL	837
LILIMANI	720	Amended (SEQ ID NO:2 538-	
HOWAIN	115) AAVPGLPSRVKOGSPOOLOGESTFAQDERECEDFALSWOCFALSTEAVALGEGSVPMEHE - (SEQ ID NO:4-539)	838 838)
MOUSE	780	TKVPGLANGVKOGSPGOLOGRSIFAGDLRLCIDEVLSWOCFGLSLLAVAVG4VVPILLHL IGEQ ID NO:6 540-	839 839)
CAT	779	AAVPGLPGHVKCGSPQQLQCRSIFAQQLRLCLDEALSWDCFGLSLLITVALGLAVPMLHHL	838
		I(SEQ ID NO:8 539-	0201
1		(SEC ID NO.0 539-	000)

SWINE	838 CGVDLWYCFHLCIAWIPHRGORRGADALFYDAFVVFDKAQSAVADWYNEIRVQLEER	395
HUMAN	839 CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWYYNELRGQLEEC 8	398
MOUSE	840 CGMDVWYCFHLCLAWLPLLARSRRSAQA-LPYDAFVVFDKAQSAVADWYNELRVRLEGR 8	898
CAT	839 CGMDLWYCFHLCLAWLPRRCRRGADALPYDAFVVFDKAQSAVADWYNELRVRLEER 8	396
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SWINE	896 RGRRALRICIEERDWIPGKTIFENIWASVYSSRKTIEVIAHTDRVSGLIRASFILAQQRL	955
HUMAN	899 RGRWALRICLEERDWILPGKTIFFENIWASVYGSRKTIFVLAHTDRVSGILRASFILLAQQRL	958
MOUSE	899 RCRRALRICLEDROWLPGQTIFENIWASIYGSRKTIFVLAHTDRVSGLIRTSFILLAQQRL	958
CAT	897 RGRRALRICIEERDWIPGKTIFENIWASVYSSRKMIFVIAHTDRVSGIIRASFILLAQQRL	956
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SWINE	956 LEDRKOVVVLVILRPDAYRSRYVRLRQRLCRQSVLLMPHQPRQQGSFWAQLGTALTRONR 10	015
HUMAN	959 LEDRKOVVVLVILSPDÆRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLÆVALTRINH 10	018
MOUSE	- 959 LEDRKDVVVLVILIRPDAHRSRYVRLRQRLCRQSVLFWPQQPNOQGGFWAQLSTALIRDNR 10	018
CAT	957 LEDRKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLMPHQPSGQRSFWAQLGTALTRDNQ 10	016
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SWINE	1016 HEYNRNFCROTTAE (SEQ ID NO:2 838-1030) Amended	030
HUMAN	1019 HEYNRNECOQP-TAE (SEQ ID NO:4 839-1032)	032
MOUSE	1019 HEYNONFORCE-TAE (SEQ ID NO:6 840-1032)	032
CAT	1017 HFYMONFCROPTTAE (SEQ ID NO:8 839-1031)	031
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